



#8

032301.190.seq.ST25.txt
SEQUENCE LISTING

<110> BATHE, Brigitte, et al.

<120> NUCLEOTIDE SEQUENCES CODING FOR THE sigD GENE

<130> 032301 WD 190

<160> 2

<170> PatentIn version 3.1

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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ggtgaaaacc cgtgaggcca aaatccaact gggatgaatta cccctgcata aatgcatgag 2
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ttg gct gat act gag cgc gag ctc gct gac ctg gta ccg cag gca acg 3
48

Met Ala Asp Thr Glu Arg Glu Leu Ala Asp Leu Val Pro Gln Ala Thr

1 5 10 15

gcg ggc gat cgt cgg gca ttg caa aga ata atg gag att att cac ccc 3
96

032301.190.seq.ST25.txt

Ala Gly Asp Arg Arg Ala Leu Gln Arg Ile Met Glu Ile Ile His Pro

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25

30

att gtt ttg cgt tat gct cgc gct cgt att gga ggt gga cgc cag cca
44

Ile Val Leu Arg Tyr Ala Arg Ala Arg Ile Gly Gly Gly Arg Gln Pro

35

40

45

acg gca gaa gac gtt gct caa gaa atc tgc ctg gcg gta gcc acc tcc
92

Thr Ala Glu Asp Val Ala Gln Glu Ile Cys Leu Ala Val Ala Thr Ser

50

55

60

att agg aac ttt gtc gac cag ggt agg ccg ttc atg gcg ttt gtc tac
40

Ile Arg Asn Phe Val Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr

65

70

75

80

ggc att gca tct aac aag gtc gca gat gct cac agg gcg atg tcg agg
88

Gly Ile Ala Ser Asn Lys Val Ala Asp Ala His Arg Ala Met Ser Arg

85

90

95

gat aaa tcg act cct att gag gaa gtc cca gaa act tca cca gat act
36

Asp Lys Ser Thr Pro Ile Glu Glu Val Pro Glu Thr Ser Pro Asp Thr

100

105

110

ttt acc ccc gaa gac ttt gcg ctg gtc agc gat gga agt aac aga gtt
84

Phe Thr Pro Glu Asp Phe Ala Leu Val Ser Asp Gly Ser Asn Arg Val

115

120

125

agg gaa ctt ctc gat cta ctg agt gaa aag gca cgc gac att ctt atc

7

B1
cont

032301.190.seq.ST25.txt

32

Arg Glu Leu Leu Asp Leu Leu Ser Glu Lys Ala Arg Asp Ile Leu Ile

130

135

140

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80

Leu Arg Val Ile Val Gly Leu Ser Ala Glu Glu Thr Ala Glu Met Val

145

150

155

160

ggc agc acc cca ggt gct gta cga gtt gcc caa cac agg gca ctc acg

28

Gly Ser Thr Pro Gly Ala Val Arg Val Ala Gln His Arg Ala Leu Thr

165

170

175

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Thr Leu Arg Ser Thr Leu Glu Gln Gln Glu Asn Lys

180

185

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<213> Corynebacterium glutamicum

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 20 25 30

Ile Val Leu Arg Tyr Ala Arg Ala Arg Ile Gly Gly Gly Arg Gln Pro
 35 40 45

Thr Ala Glu Asp Val Ala Gln Glu Ile Cys Leu Ala Val Ala Thr Ser
 50 55 60

Ile Arg Asn Phe Val Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr
 65 70 75 80

Gly Ile Ala Ser Asn Lys Val Ala Asp Ala His Arg Ala Met Ser Arg
 85 90 95

Asp Lys Ser Thr Pro Ile Glu Glu Val Pro Glu Thr Ser Pro Asp Thr
 100 105 110

Phe Thr Pro Glu Asp Phe Ala Leu Val Ser Asp Gly Ser Asn Arg Val
 115 120 125

Arg Glu Leu Leu Asp Leu Leu Ser Glu Lys Ala Arg Asp Ile Leu Ile
 130 135 140

Leu Arg Val Ile Val Gly Leu Ser Ala Glu Glu Thr Ala Glu Met Val
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Gly Ser Thr Pro Gly Ala Val Arg Val Ala Gln His Arg Ala Leu Thr
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Thr Leu Arg Ser Thr Leu Glu Gln Gln Glu Asn Lys
 180 185